What is claimed is:

1. A method for inhibiting replication or transcription of a nucleic acid molecule indicative of a disease state, the method comprising:

targeting the nucleic acid molecule with an oligonucleotide; and,

binding of the oligonucleotide to the target nucleic acid molecule; and,

wrapping around the target nucleic acid molecule; thereby,

inhibiting transcription of the target nucleic acid molecule.

2. The method of claim 1, wherein the oligonucleotide comprises a backbone nucleic acid sequence, an arm nucleic acid sequence.

3. The method of claim 2, wherein the oligonucleotide comprises a double stranded nucleic acid sequence.

4. The method of claim 2, wherein the oligonucleotide comprises a single stranded nucleic acid sequence.

5. The method of claim 2, wherein the backbone and arms are complementary to a target nucleic acid molecule.

6. The method of claim 5, wherein the nucleic acid sequences of the arms are complementary to the backbone nucleic acid sequences.

7. The method of claim 6, wherein a 5' to 3' nucleic acid sequence comprising the arm is complementary to a 3' to 5'nucleic acid sequence comprising the backbone.

8. The method of claim 5, wherein a 3' to 5' nucleic acid sequence comprising the arm is complementary to a 5' to 3'nucleic acid sequence comprising the backbone.

9. The method of claims 7 or 8, wherein the 5' to 3' arm and the 3' to 5' arm comprise an equal ratio of nucleic acid bases.

10. The method of claims 7 or 8 wherein the 5' to 3' arm and the 3' to 5' arm comprise a varying ratio of nucleic acid bases.

11. The method of claim 10 wherein the ratio of nucleic acid bases of the 5' to 3' arm and the 3' to 5' arm vary between about 0.1 : 1 to about 20:1.

12. The method of claim 2 wherein the backbone comprises at least one mismatching base compared to the arm having a complementary nucleic acid sequence.

13. The method of claim 2 wherein the backbone comprises at least one mismatching base compared to the target nucleic acid molecule it is designed to detect.

14. The method of claim 2 wherein the oligonucleotide invades a double stranded molecule in the region of the target sequence by denaturing the bonds between the complementary target sequences of the double stranded molecule.

15. The method of claim 2 wherein the oligonucleotide has equal or higher specificity and affinity for a target oligonucleotide sequence than the complementary target oligonucleotide sequence.

16. The method of claim 15, wherein the association constant (K_a) of the oligonucleotide for the target nucleic acid molecule is higher than the association constant of the complementary strands of a double stranded molecule.

17. The method of claim 15, wherein the association constant (K_a) of the oligonucleotide for the target nucleic acid molecule is higher than a disassociation constant (K_d) of the complementary strand of the target sequence in a double stranded molecule.

18. The method of claim 15, wherein the oligonucleotide can bind to a wild type gene sequence and any alleles or variants thereof.

19. The method of claim 1, wherein the oligonucleotide binds to single-stranded DNA targets.

20. The method of claim 1, wherein the oligonucleotide hybridizes with double-stranded DNA target molecules as well as messenger RNA and/or RNA secondary structures.

21. The method of claim 1, wherein the oligonucleotide hybridizes with genomic target molecules as well as episomal structures.

22. The method of claims 20 or 21, wherein the 5' arm ligates to the 3' arm after the oligonucleotide has hybridized to its target nucleic acid molecule thereby forming a locked complex.

23. The method of claim 22, wherein the 5' and 3' arms are ligated by native cellular ligases.

24. The method of claim 22, wherein 5' and 3' ends of the oligonucleotide are chemically modified such that they self-ligate when the ends are juxtaposed on their specific target.

25. The method of claim 22, wherein the locked complex inhibits replication of the nucleic acid sequence.

26. The method of claim 22, wherein the locked complex inhibits transcription.

27. The method of claims 25 or 26 wherein the locked complex inhibits replication and/or transcription *in vitro* or *in vivo*.

28. The method of claim 27, wherein the oligonucleotide selectively inhibits replication and/or transcription of a cell comprising the target nucleic acid molecule.

29. The method of claim 28, wherein the target nucleic acid molecule in a cell is expressed in a disease state or is a foreign nucleic acid molecule.

30. The method of claim 28, wherein the disease state is cancer.

31. The method of claim 28, wherein the foreign nucleic acid molecule is from an infectious disease organism.

32. The method of claim 29, wherein the infectious disease organism is virus, bacteria, protozoa or fungi.

33. The method of claim 32, wherein the bacterium is a multi-drug resistant bacterium.

34. The method of any one of claims 1 through 33, wherein the oligonucleotide comprises a total of from about 8 to about 200 base units.

35. The method of any one of claims 1 through 33, wherein the oligonucleotide comprises a total of from about 8 to about 150 base units.

36. The method of any one of claims 1 through 33, wherein the oligonucleotide comprises a total of from about 10 to about 100 base units.

37. The method of any one of claims 1 through 33, wherein the oligonucleotide comprises a total of from about 10 to about 60 base units.

38. The method of any one of claims 1 through 33, wherein the oligonucleotide comprises modified base units.

39. The method of claim 38 wherein the modified bases comprise phosphorthiorate, methylphosphonate, peptide nucleic acids, and/or LNA molecules.

40. The method of claim 39 wherein the oligonucleotide comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9,10, or comprises only modified base units.

41. A method for selectively treating cells comprising an infectious disease organism, comprising:

administering to the cells an oligonucleotide sequence that is complementary to a target nucleic acid molecule of an infectious disease organism, the cells comprising an oligonucleotide sequence of an infectious disease organism; wherein,

the oligonucleotide wraps around the target nucleic acid molecule; and,

inhibiting transcription of the target nucleic acid molecule.

42. The method of claim 41, wherein the cells are mammalian or plant cells.

43. The method of any one of claims 41 or 42, wherein the cells are infected with a virus bacteria, protozoa or fungi.

44. The method of any one of claims 41 through 43, wherein the cells are in any one of G1, S, M, or G2 stage of a cell cycle.

45. The method of any one of claims 41 through 43, wherein the oligonucleotide binds to a wild type infectious disease organisms' target gene sequence and any alleles or variants thereof.

46. The method of claim 45, wherein the oligonucleotide binds to single-stranded DNA targets.

47. The method of claim 45, wherein the oligonucleotide hybridizes with double-stranded DNA target molecules as well as messenger RNA and/or RNA secondary structures.

48. The method of claim 45, wherein the oligonucleotide hybridizes with genomic target molecules as well as episomal structures.

49. The method of claim 45, wherein the 5' end of the oligonucleotide and the 3' end of the oligonucleotide wrap around the target nucleic acid molecule after

the oligonucleotide has hybridized to its target nucleic acid molecule thereby forming a helix.

50. The method of claim 49, wherein the 5' end of the oligonucleotide ligates to the 3' end of the oligonucleotide after formation of the helix, forming a locked complex.

51. The method of claim 49, wherein the locked complex inhibits replication of the target nucleic acid sequence.

52. The method of claim 49, wherein the locked complex inhibits transcription.

53. The method of any one of claims 41 through 52, wherein the oligonucleotide comprises modified base units.

54. The method of claim 53, wherein the modified bases comprise phosphorthiorate, methylphosphonate, peptide nucleic acids, and/or LNA molecules.

55. The method of claim 53, wherein the oligonucleotide comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9,10, or comprises only modified base units.

56. The method of claim 53, wherein the oligonucleotide comprising the modified units has a higher association constant (K_a) for the target nucleic acid molecule than the association constant of the complementary strands of a double stranded molecule.

57. The method of claim 53, wherein the association constant (K_a) of the oligonucleotide for the target nucleic acid molecule is higher than a disassociation constant (K_d) of the complementary strand of the target sequence in a double stranded molecule.

56. The method of any one of claims 53 through 57, wherein the oligonucleotide can bind to a wild type target gene sequence and any alleles or variants thereof.

57. The method of any one of claims 41 through 56, wherein the oligonucleotide is comprised of a double stranded nucleic acid sequence.

58. The method of any one of claims 41 through 56, wherein the oligonucleotide is comprised of a single stranded nucleic acid sequence.

59. A method for treating a mammal suffering from or susceptible to an infectious disease or cancer, the method comprising:

administering to the mammal a therapeutically effective amount of an oligonucleotide.

60. The method of claim 59, wherein the infectious disease is caused by or associated with a virus, bacteria, protozoa or fungi.

61. The method of claim 59, wherein the infectious agent is present in any tissue or organ of a mammal.

62. The method of any one of claims 59 through 61, wherein the disease or disorder is associated with undesired expression of at least a portion of a sequence identified in tables 1, 2, 4, 5 or 6 above, or variants thereof.

63. The method of any one of claims 59 through 62, wherein the administered oligonucleotide hybridizes with messenger RNA of the gene to inhibit expression thereof.

64. The method of any one of claims 59 through 61, wherein administering the oligonucleotide results in inhibition of gene expression.

65. The method of any one of claims 59 through 61, wherein the virus is HPV.

66. The method of claim 65 wherein the oligonucleotide that targets the HPV is identified by SEQ. ID. NO 2.